



UTHou-16UTL final.ST25  
SEQUENCE LISTING

<110> Board of Regents of the University of Texas System

<120> MUTATIONS IN A NOVEL PHOTORECEPTOR-PINEAL GENE ON 17P CAUSE LEBER  
CONGENITAL AMAUROSIS (LCA4)

<130> 96606/16UTL

<140> 09/765,061

<141> 2001-01-17

<150> 60/331362

<151> 2001-01-14

<160> 82

<170> PatentIn version 3.3

<210> 1

<211> 6689

<212> DNA

<213> Homo sapiens

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<221> gene

<222> (1)..(6689)

<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting  
protein-like 1

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<221> misc\_feature

<222> (1897)..(1906)

<223> n is a, c, g, or t

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<222> (3946)..(3946)

<223> n is a, c, g, or t

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<211> 1119

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<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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protein-like 1

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 <213> Bos taurus

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 <223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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<220>  
<221> gene  
<222> (1)..(925)  
<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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<213> Mus musculus

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<221> gene

<222> (1)..(1075)

<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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aggttgggtg ggagctgcgg gttgaacctt ggggcgaggg ctggggctat ggact          1075

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<210> 7

<211> 1179

<212> DNA

<213> Macaca mulatta

<220>

<221> gene

<222> (1)..(1179)

<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

UTHou-16UTL final.ST25

<400> 7

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atggatgccg ctctgctcct gaacgtggaa ggggtcaaga aaaccattct gcacggaggc      60
acgggcgagc tcccaaactt catcaccgga tcccagtgga tctttcattt ccgcaccatg      120
aaatgtgatg aggagcgcac ggtcatcgac gacagccgtc aggtggacca gcccatgcac      180
atcatcatcg ggaacatgtt caagctcgag gtctgggaga tcttgcacac ctccatgagg      240
gtgcacgagg tggccgagtt ctggtgcgac accatccaca cgggggtcta ccccatyctg      300
tcccggagcc tgcggcagat ggcccagggc aaggaccca cggagtggca cgtgcacaca      360
tgcgggctgg ccaacatgtt cgcctaccac acgctgggct acgaggacct ggacgagctg      420
cagaaggagc ctcagcctct gatctttgtg atcgagctgc tgcaggttga cgccccgagt      480
gattaccaga gggagacctg gaacctgagc aatcatgaga agatgaaggt ggtgcccgct      540
ctccacggag agggaaatcg gctcttcaag ytgggccgct acgaggaggc ctcttccaag      600
taccaggagg ccatcatctg cctaaggaac ctgcagacca aggagaagcc gtgggaggtg      660
cagtggctga agctggagaa gatgatcaac accctgacct tcaactactg ccagtgcctg      720
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ccaggcatcg tgaaggccta ctatgtgcgt gcccgggctc acgcggagggt gtggaacgag      840
gccgaggcca aggcggacct ccagaaagtg ctggagctgg agccatccat gcagaaggcg      900
gtgcgcaggg agctgaggct gctggagaac cgcattggcg agaagcagga ggaggagagg      960
ctgcgctgcc ggaacatgct gagccaggga gccacgcagc ctcccgaga gccaccggca     1020
cagcccccca cagcaccacc tgcagagctg tccacagggc cacctgcgga cccaccggcg     1080
gagcccccca cagcaccacc tgcggagctg tccacagggc cacctgcaga gccaccggca     1140
gagctcccc tgtccccagg gcactcactg cagcactga                                1179

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<210> 8

<211> 1119

<212> DNA

<213> Saimiri sciureus

<220>

<221> gene

<222> (1)..(1119)

<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

<400> 8

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acgggcgagc tcccaaattt catcaccgga tcccagtgga tctttcattt ccgcaccatg      120

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UTHou-16UTL final.ST25

aaatgtgatg aggagcggac ggtgattgac gacagcaggg aggtgggcca gcccatgcac	180
atcatcatcg ggaacatggt caagctggag gtctgggaga tcttgcctac gtccatgcgg	240
gtgcgagagg tggccgagtt ctggtgcgac accatccaca cgggggtcta ccccatcctg	300
tcccggagcc tgcggcagat ggcccagggc aaggacccga cggagtggca tgtgcacacg	360
tgcgggctgg ccaacatggt cgcctaccac acgctgggct acgaggacct ggatgagctg	420
cagaaggagc ctcagcctct gatctttgtg atcgagctgc tgcaggttga tgccccaagt	480
gattaccaga gggagacctg gaacctgagc aatcacgaga agatgaagggt ggtgcccgtc	540
ctccatggag aaggaaatag gctcttcaag ctgggccgct acgaggaggc ctcttccaag	600
taccaggagg ccatcatctg cctaaggaac ctgcagacca aggagaaacc ctgggaggtg	660
cagtggctga agctggagaa gatgatcaat accctgatcc tcaactactg tcagtgtctg	720
ctgaagaagg aggagtacta cgaggctctg gagcatacca gtgacattct ccggcaccac	780
ccaggcattg tgaaggccta ctatgtgcgc gcccgggctc acgcggaggt gtggaacgag	840
gccgaggcca aggcggacct ccagaaagtg ctggagctgg agccgtccat gcagaaggcg	900
gtgcgcaggg agctgaggct gctggagaac cgcattggcg agaagcagga ggaggagcgg	960
ctgcgctgcc gcaacatgct gagccagggg gccacgtggt cccccgcgga gccacccgca	1020
gagccacctg cagagtcac caccagagcca cccgcagagc cacctgcaga gccacctgca	1080
gagctaacct tgaccccggt gcaccacta cagcactga	1119

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 <213> Homo sapiens

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 <223> Amino Acid codon position 79: Met to Thr mutation

<400> 9  
 acctccacgc gggtg 15

<210> 10  
 <211> 15  
 <212> DNA  
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<220>  
 <221> mutation  
 <222> (7)..(9)

<223> Amino Acid condon 88 mutation: Trp to X

<400> 10

gagttctgat gcgac

15

<210> 11

<211> 15

<212> DNA

<213> Homo sapiens

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<221> mutation

<222> (7)..(9)

<223> Amino Acid condon 96 mutation: Val to Ile mutation

<400> 11

acggggatct acccc

15

<210> 12

<211> 15

<212> DNA

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<223> Amino Acid codon 124 mutation: Thr to Ile mutation

<400> 12

gaccccatag agtgg

15

<210> 13

<211> 15

<212> DNA

<213> Homo sapiens

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<221> mutation

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<223> Amino Acid codon 376 mutation: Pro to Ser mutation

<400> 13

ccaccctcgt ccca

15

<210> 14

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

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<222> (7)..(9)  
 <223> Amino Acid codon 163 mutation: Gln to X mutation

<400> 14  
 gattactaga gggag 15

<210> 15  
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 <223> Amino Acid codon 197 mutation: Ala to Pro mutation

<400> 15  
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<210> 16  
 <211> 15  
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 <223> Amino Acid codon 278 mutation: Trp to X mutation

<400> 16  
 gaggtgtgaa atgag 15

<210> 17  
 <211> 15  
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<220>  
 <221> mutation  
 <222> (7)..(7)  
 <223> a to g mutation: IVS2-2A to G

<400> 17  
 tccccacggc acacg 15

<210> 18  
 <211> 15  
 <212> DNA  
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<220>

<221> mutation  
 <222> (7)..(9)  
 <223> Amino Acid codon 262 mutation: Glu to Ser

<400> 18  
 cacccaagtg cgcgg 15

<210> 19  
 <211> 15  
 <212> DNA  
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<220>  
 <221> mutation  
 <222> (7)..(9)  
 <223> Amino Acid codon 302 mutation: Arg to Leu

<400> 19  
 gcggtgctca gggag 15

<210> 20  
 <211> 13  
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<220>  
 <221> mutation  
 <222> (5)..(5)  
 <223> Deletion of "tgcagagccacc" at location 5

<400> 20  
 gccacccaca gca 13

<210> 21  
 <211> 15  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> mutation  
 <222> (7)..(9)  
 <223> Amino Acid codon 239 mutation: Cys to Arg

<400> 21  
 tgccagcgcc tgctg 15

<210> 22  
 <211> 13  
 <212> DNA  
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<220>  
 <221> mutation  
 <222> (5)..(5)  
 <223> two base deletion at location 5: "ag"  
  
 <400> 22  
 tcccgcagcc acc 13

<210> 23  
 <211> 15  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> mutation  
 <222> (7)..(9)  
 <223> Amino Acid codon 42 mutation: Cys to X  
  
 <400> 23  
 atgaaatgag atgag 15

<210> 24  
 <211> 12  
 <212> DNA  
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<220>  
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 <222> (7)..(7)  
 <223> nine base deletion at location 7: "ctccggcac"  
  
 <400> 24  
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<210> 25  
 <211> 21  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (7)..(7)  
 <223> eight base insertion: "gtgatctt"  
  
 <400> 25  
 gactaggtga tcttgtgatc t 21

<210> 26  
 <211> 12  
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<220>  
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 <222> (4)..(4)  
 <223> g to a polymorphism: IVS1-9 g to a benign mutation

<400> 26  
 ctcagtgact ag 12

<210> 27  
 <211> 12  
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<220>  
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 <223> g to c polymorphism: IVS2+66G to C Benign

<400> 27  
 tttgccgggc tg 12

<210> 28  
 <211> 12  
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<220>  
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 <222> (4)..(4)  
 <223> c to t polymorphism: IVS2-88C to T Benign

<400> 28  
 tcctctcagg ag 12

<210> 29  
 <211> 12  
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<220>  
 <221> mutation  
 <222> (4)..(4)  
 <223> g to a polymorphism: IVS2-14G to A Benign

<400> 29  
 atccatttat cc 12

<210> 30  
 <211> 12  
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<220>  
 <221> mutation  
 <222> (4)..(4)  
 <223> a to c mutation: IVS2-10A to C Benign

<400> 30  
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12

<210> 31  
 <211> 12  
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<220>  
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 <223> t to c mutation: IVS3-25T to C Benign

<400> 31  
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12

<210> 32  
 <211> 12  
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<220>  
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<400> 32  
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12

<210> 33  
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<220>  
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 <222> (7)..(7)  
 <223> g to a mutation: IVS5+18G to A Benign

<400> 33  
 aggagcggac ag

12

<210> 34  
 <211> 12  
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<213> Homo sapiens

<220>

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<222> (7)..(9)

<223> Amino Acid codon mutation: Asp 90 His Benign

<400> 34

tggtgccaca cc

12

<210> 35

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid mutation: Phe 37 Phe Benign

<400> 35

catttccgca cc

12

<210> 36

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid mutation: Ser 78 Ser Benign

<400> 36

acctctatgc gg

12

<210> 37

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid mutation: Cys 89 Cys Benign

<400> 37

tggtgtgaca cc

12

<210> 38

<211> 12

<212> DNA  
<213> Homo sapiens

<220>  
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<223> Amino Acid codon mutation: Leu 100 Leu Benign

<400> 38  
atcctgtccc gg 12

<210> 39  
<211> 12  
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<222> (4)..(6)  
<223> Amino Acid codon mutation: His 172 His

<400> 39  
aatcacgaga ag 12

<210> 40  
<211> 12  
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<220>  
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<223> Amino Acid codon mutation: Pro 217 Pro Benign

<400> 40  
aagccgtggg ag 12

<210> 41  
<211> 12  
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<220>  
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<223> Amino Acid codon mutation: Asp 255 Asp Benign

<400> 41  
agtgacattc tc 12

<210> 42

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<211> 20  
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<220>  
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 <222> (1)..(20)  
 <223> PCR primer 1 page 57

<400> 42  
 aagaaaacca ttctgcacgg 20

<210> 43  
 <211> 19  
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 <213> Homo sapiens

<220>  
 <221> primer  
 <222> (1)..(19)  
 <223> PCR primer 2 page 57

<400> 43  
 tgcagctcgt ccaggtcct 19

<210> 44  
 <211> 17  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> primer  
 <222> (1)..(17)  
 <223> PCR primer 1 page 58

<400> 44  
 gacacctccc tttctcc 17

<210> 45  
 <211> 18  
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 <213> Homo sapiens

<400> 45  
 gctggggctg cctggctg 18

<210> 46  
 <211> 20  
 <212> DNA  
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<220>  
 <221> primer  
 <222> (1)..(20)  
 <223> PCR primer 3 page 58

<400> 46  
 ccgagtgatt accagagggga 20

<210> 47  
 <211> 20  
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 <213> Homo sapiens

<220>  
 <221> primer  
 <222> (1)..(20)  
 <223> PCR primer 4 page 58

<400> 47  
 tgagctccag cacctcatag 20

<210> 48  
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 <212> DNA  
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<220>  
 <221> primer  
 <222> (1)..(18)  
 <223> PCR primer 1 page 60

<400> 48  
 acgcagaggt gtggaatg 18

<210> 49  
 <211> 19  
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 <213> Homo sapiens

<220>  
 <221> primer  
 <222> (1)..(19)  
 <223> PCR primer 2 page 60

<400> 49  
 aaaaagtgac accacgatc 19

<210> 50  
 <211> 34  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)..(34)  
 <223> exon - donor splice site 1 of Table 1 page 49  
 CGGATCCCGAgtagtgaggccctccggagcaga

<400> 50  
 cgg atc ccg agt gag tgg ggc cct ccg gag cag a  
 Arg Ile Pro Ser Glu Trp Gly Pro Pro Glu Gln  
 1 5 10

34

<210> 51  
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<220>  
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 <222> (1)..(35)  
 <223> exon - acceptor splice site 1 of Table 1 page 49  
 cagagtgcaccgtctcggtgactagGTGATCTTTC

<400> 51  
 cag agt gca ccg tct cgg tga cta ggt gat ctt tc  
 Gln Ser Ala Pro Ser Arg Leu Gly Asp Leu  
 1 5 10

35

<210> 52  
 <211> 35  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)..(35)  
 <223> exon - donor splice site 2 of Table 1 page 49

CSACACCATCgtaagtaggccctgcgcgcctgtct

<400> 52  
 csa cac cat cgt aag tag gcc ctg cgc gcc tgt ct  
 Xaa His His Arg Lys Ala Leu Arg Ala Cys  
 1 5 10

35

<210> 53  
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<220>  
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<223> exon - acceptor splice site 2 of Table 1 page 49

gccatccatccgtttatccccacagCACACGGGGG

<400> 53

gcc atc cat ccg ttt atc ccc aca gca cac ggg gg

35

Ala Ile His Pro Phe Ile Pro Thr Ala His Gly

1 5 10

<210> 54

<211> 35

<212> DNA

<213> Homo sapiens

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<222> (1)..(35)

<223> exon - donor splice site 3 of Table 1 page 49

GCTGCTGCAGgtggggctgggggttggcagggctgg

<400> 54

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35

Ala Ala Ala Gly Gly Ala Gly Val Gly Arg Ala

1 5 10

<210> 55

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - acceptor splice site 3 of Table 1 page 49

cactgacctgcagctctggggccagGTTGATGCCC

<400> 55

cac tga cct gca gct ctg ggg cca ggt tga tgc cc

35

His Pro Ala Ala Leu Gly Pro Gly Cys

1 5

<210> 56

<211> 35

<212> DNA

<213> Homo sapiens

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<221> exon

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<223> exon - donor splice site 4 of Table 1 page 49

GCAGACCAAGgtcagaggccgctggccacggggtg

<400> 56

gca gac caa ggt cag agg ccg ctg gcc acg ggg tg  
Ala Asp Gln Gly Gln Arg Pro Leu Ala Thr Gly  
1 5 10

35

<210> 57

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - acceptor splice site 4 of Table 1 page 49

catggctgaccttctccctgggcagGAGAAGCCRT

<400> 57

cat ggc tga cct tct ccc tgg gca gga gaa gcc rt  
His Gly Pro Ser Pro Trp Ala Gly Glu Ala  
1 5 10

35

<210> 58

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - donor splice site 5 of Table 1 page 49

CACCACCCAGgtgcgcggggctgcaggggaggaca

<400> 58

cac cac cca ggt gcg cgg ggc tgc agg ggc gga ca  
His His Pro Gly Ala Arg Gly Cys Arg Gly Gly  
1 5 10

35

<210> 59

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - acceptor splice site 5 of Table 1 page 49

gctggatgctccctgctccccacagGCATCGTGAA



<400> 59  
gct gga tgc tcc ctg ctc ccc aca ggc atc gtg aa 35  
Ala Gly Cys Ser Leu Leu Pro Thr Gly Ile Val  
1 5 10

<210> 60  
<211> 18  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (1)..(18)  
<223> PCR Primer 1 for AIPL1 fragment amplification Table 5 page 61

<400> 60  
ggacacctcc ctttctcc 18

<210> 61  
<211> 18  
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<220>  
<221> primer  
<222> (1)..(18)  
<223> PCR Primer 2 for AIPL1 fragment amplification Table 5 page 61

<400> 61  
gctggggctg cctggctg 18

<210> 62  
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<212> DNA  
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<220>  
<221> primer  
<222> (1)..(20)  
<223> PCR Primer 3 for AIPL1 fragment amplification Table 5 page 61

<400> 62  
gggccttgaa cagtgtgtct 20

<210> 63  
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<220>  
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<222> (1)..(19)  
 <223> PCR Primer 4 for AIPL1 fragment amplification Table 5 page 61  
 <400> 63  
 tttcccgaac cacagcagc 19

<210> 64  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> primer  
 <222> (1)..(18)  
 <223> PCR Primer 5 for AIPL1 fragment amplification Table 5 page 61  
 <400> 64  
 agtgaggag caggattc 18

<210> 65  
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<220>  
 <221> primer  
 <222> (1)..(20)  
 <223> PCR Primer 6 for AIPL1 fragment amplification Table 5 page 61  
 <400> 65  
 tgcccatgat gcccgctgtc 20

<210> 66  
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<220>  
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 <223> PCR Primer 7 for AIPL1 fragment amplification Table 5 page 61  
 <400> 66  
 tttcgggtct ctgatggg 18

<210> 67  
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 <212> DNA  
 <213> Homo sapiens

<220>

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<221> primer
<222> (1)..(17)
<223> PCR Primer 8 for AIPL1 fragment amplification Table 5 page 61

<400> 67
gcaggctccc cagagtc                                     17

<210> 68
<211> 19
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(19)
<223> PCR Primer 9 for AIPL1 fragment amplification Table 5 page 61

<400> 68
gcagctgcct caggtcatg                                     19

<210> 69
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> primer
<222> (1)..(18)
<223> PCR Primer 10 for AIPL1 fragment amplification Table 5 page 61

<400> 69
gtggggtgga aagaaaag                                     18

<210> 70
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> primer
<222> (1)..(18)
<223> PCR Primer 11 for AIPL1 fragment amplification Table 5 page 61

<400> 70
ctgggaaggg agctgtag                                     18

<210> 71
<211> 19
<212> DNA
<213> Homo sapiens

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<220>  
 <221> primer  
 <222> (1)..(19)  
 <223> PCR Primer 12 for AIPL1 fragment amplification Table 5 page 61

<400> 71  
 aaaagtgaca ccacgatcc

19

<210> 72  
 <211> 384  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(384)  
 <223> Human AIPL1 Protein

<400> 72

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile  
 1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg  
 20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val  
 35 40 45

Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His Ile Ile Ile Gly  
 50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg  
 65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val  
 85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp  
 100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala  
 115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro  
 130 135 140

Gln Pro Leu Val Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser

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145		150		155		160									
Asp	Tyr	Gln	Arg	Glu	Thr	Trp	Asn	Leu	Ser	Asn	His	Glu	Lys	Met	Lys
				165					170					175	
Ala	Val	Pro	Val	Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Phe	Lys	Leu	Gly
			180					185					190		
Arg	Tyr	Glu	Glu	Ala	Ser	Ser	Lys	Tyr	Gln	Glu	Ala	Ile	Ile	Cys	Leu
		195					200					205			
Arg	Asn	Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Gln	Trp	Leu	Lys
	210					215					220				
Leu	Glu	Lys	Met	Ile	Asn	Thr	Leu	Ile	Leu	Asn	Tyr	Cys	Gln	Cys	Leu
225					230					235					240
Leu	Lys	Lys	Glu	Glu	Tyr	Tyr	Glu	Val	Leu	Glu	His	Thr	Ser	Asp	Ile
			245					250						255	
Leu	Arg	His	His	Pro	Gly	Ile	Val	Lys	Ala	Tyr	Tyr	Val	Arg	Ala	Arg
			260					265					270		
Ala	His	Ala	Glu	Val	Trp	Asn	Glu	Ala	Glu	Ala	Lys	Ala	Asp	Leu	Gln
		275					280					285			
Lys	Val	Leu	Glu	Leu	Glu	Pro	Ser	Met	Gln	Lys	Ala	Val	Arg	Arg	Glu
	290					295					300				
Leu	Arg	Leu	Leu	Glu	Asn	Arg	Met	Ala	Glu	Lys	Gln	Glu	Glu	Glu	Arg
305					310					315					320
Leu	Xaa	Cys	Arg	Asn	Met	Leu	Ser	Gln	Gly	Ala	Thr	Gln	Pro	Pro	Ala
				325					330					335	
Glu	Pro	Pro	Thr	Glu	Pro	Pro	Ala	Gln	Ser	Ser	Thr	Glu	Pro	Pro	Ala
			340					345					350		
Glu	Pro	Pro	Thr	Ala	Pro	Ser	Ala	Glu	Leu	Ser	Ala	Gly	Pro	Pro	Ala
		355					360					365			
Glu	Pro	Ala	Thr	Glu	Pro	Pro	Pro	Ser	Pro	Gly	His	Ser	Leu	Gln	His
	370					375					380				

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<210> 73  
 <211> 384  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> Peptide  
 <222> (1)..(384)  
 <223> Chimpanzee AIPL1 Protein

<400> 73

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile  
 1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg  
 20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val  
 35 40 45

Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His Ile Ile Ile Gly  
 50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg  
 65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val  
 85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp  
 100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala  
 115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro  
 130 135 140

Gln Pro Leu Val Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser  
 145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys  
 165 170 175

Ala Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly  
 180 185 190

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Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu  
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys  
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu  
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile  
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg  
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Arg  
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg  
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala  
325 330 335

Glu Pro Pro Thr Glu Pro Pro Ala Gln Ser Ser Thr Glu Pro Pro Ala  
340 345 350

Glu Pro Pro Pro Ala Pro Ser Ala Glu Leu Ser Ala Gly Pro Pro Ala  
355 360 365

Glu Thr Ala Thr Glu Pro Pro Pro Ser Pro Gly His Ser Leu Gln His  
370 375 380

<210> 74  
<211> 372  
<212> PRT  
<213> Papio anubis

<220>  
<221> peptide  
<222> (1)..(372)

&lt;223&gt; Baboon AIPL1 Protein

&lt;400&gt; 74

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Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1          5          10          15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
          20          25          30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
          35          40          45

Ile Asp Asp Ser Arg Gln Val Asp Gln Pro Met His Ile Ile Ile Gly
50          55          60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65          70          75          80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
          85          90          95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
          100          105          110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
          115          120          125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
          130          135          140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145          150          155          160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
          165          170          175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
          180          185          190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
          195          200          205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210          215          220

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UTHou-16UTL final.ST25

Leu Glu Lys Met Ile Asn Thr Leu Thr Leu Asn Tyr Cys Gln Cys Leu  
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile  
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg  
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln  
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg  
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Thr  
325 330 335

Glu Pro Pro Ala Glu Pro His Thr Ala Pro Pro Ala Glu Leu Ser Thr  
340 345 350

Gly Pro Pro Ala Glu Pro Pro Ala Glu Leu Pro Leu Ser Pro Gly His  
355 360 365

Ser Leu Gln His  
370

<210> 75  
<211> 328  
<212> PRT  
<213> Bos taurus

<400> 75

Met Asp Ala Thr Leu Leu Leu Asn Val Glu Gly Ile Lys Lys Thr Ile  
1 5 10 15

Leu His Gly Gly Thr Gly Asp Leu Pro Asn Phe Ile Thr Gly Ala Arg  
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val  
35 40 45

UTHou-16UTL final.ST25

Ile	Asp	Asp	Ser	Lys	Gln	Val	Gly	His	Pro	Met	His	Ile	Ile	Ile	Gly	50	55	60
Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu	Leu	Thr	Ser	Met	Arg	65	70	75
Val	Ser	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp	Thr	Ile	His	Thr	Gly	Val	85	90	95
Tyr	Pro	Ile	Leu	Ser	Arg	Ser	Leu	Arg	Gln	Met	Ala	Glu	Gly	Lys	Asp	100	105	110
Pro	Thr	Glu	Trp	His	Val	His	Thr	Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala	115	120	125
Tyr	His	Thr	Leu	Gly	Tyr	Glu	Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro	130	135	140
Gln	Pro	Leu	Ile	Phe	Ile	Ile	Glu	Leu	Leu	Gln	Val	Glu	Ala	Pro	Ser	145	150	155
Gln	Tyr	Gln	Arg	Glu	Thr	Trp	Asn	Leu	Asn	Asn	Gln	Glu	Lys	Met	Gln	165	170	175
Ala	Val	Pro	Ile	Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Phe	Lys	Leu	Gly	180	185	190
Arg	Tyr	Glu	Glu	Ala	Ser	Asn	Lys	Tyr	Gln	Glu	Ala	Ile	Val	Cys	Leu	195	200	205
Arg	Asn	Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Gln	Trp	Leu	Lys	210	215	220
Leu	Glu	Lys	Met	Ile	Asn	Thr	Leu	Ile	Leu	Asn	Tyr	Cys	Gln	Cys	Leu	225	230	235
Leu	Lys	Lys	Glu	Glu	Tyr	Tyr	Glu	Val	Leu	Glu	His	Thr	Ser	Asp	Ile	245	250	255
Leu	Arg	His	His	Pro	Gly	Ile	Val	Lys	Ala	Tyr	Tyr	Val	Arg	Ala	Arg	260	265	270
Ala	His	Ala	Glu	Val	Trp	Asn	Glu	Ala	Glu	Ala	Lys	Ala	Asp	Leu	Glu	275	280	285

UTHou-16UTL final.ST25

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Gln Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Asn Arg Leu Glu Glu Lys Arg Glu Glu Glu Arg  
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Gly  
325

<210> 76  
<211> 328  
<212> PRT  
<213> Mus musculus

<220>  
<221> peptide  
<222> (1)..(328)  
<223> Mouse AIPL1 Protein

<400> 76

Met Asp Val Ser Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile  
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg  
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val  
35 40 45

Ile Asp Asp Ser Lys Gln Val Gly Gln Pro Met Ser Ile Ile Ile Gly  
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Thr Leu Leu Thr Ser Met Arg  
65 70 75 80

Leu Gly Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val  
85 90 95

Tyr Pro Met Leu Ser Arg Ser Leu Arg Gln Val Ala Glu Gly Lys Asp  
100 105 110

Pro Thr Ser Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala  
115 120 125

UTHou-16UTL final.ST25

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro  
130 135 140

Gln Pro Leu Val Phe Leu Tyr Glu Leu Leu Gln Val Glu Ala Pro Asn  
145 150 155 160

Glu Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Glu Glu Arg Met Gln  
165 170 175

Ala Val Pro Leu Leu His Gly Glu Gly Asn Arg Leu Tyr Lys Leu Gly  
180 185 190

Arg Tyr Asp Gln Ala Ala Thr Lys Tyr Gln Glu Ala Ile Val Cys Leu  
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Glu Trp Leu Lys  
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu  
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile  
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Met Arg Ala Arg  
260 265 270

Ala His Ala Glu Val Trp Asn Ala Glu Glu Ala Lys Ala Asp Leu Glu  
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Leu Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Ser Arg Leu Ala Asp Lys Gln Glu Glu Glu Arg  
305 310 315 320

Gln Arg Cys Arg Ser Met Leu Gly  
325

<210> 77  
<211> 392  
<212> PRT  
<213> Macaca mulatta

<220>

UTHou-16UTL final.ST25

<221> peptide

<222> (1)..(392)

<223> Rhesus Monkey AILP1 Protein

<400> 77

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile  
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg  
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val  
35 40 45

Ile Asp Asp Ser Arg Gln Val Asp Gln Pro Met His Ile Ile Ile Gly  
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg  
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val  
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp  
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala  
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro  
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser  
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys  
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly  
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu  
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys

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210

215

220

Leu Glu Lys Met Ile Asn Thr Leu Thr Leu Asn Tyr Cys Gln Cys Leu  
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile  
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg  
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln  
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg  
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala  
325 330 335

Glu Pro Pro Ala Gln Pro Pro Thr Ala Pro Pro Ala Glu Leu Ser Thr  
340 345 350

Gly Pro Pro Ala Asp Pro Pro Ala Glu Pro Pro Thr Ala Pro Pro Ala  
355 360 365

Glu Leu Ser Thr Gly Pro Pro Ala Glu Pro Pro Ala Glu Leu Pro Leu  
370 375 380

Ser Pro Gly His Ser Leu Gln His  
385 390

<210> 78  
<211> 372  
<212> PRT  
<213> Saimiri sciureus

<220>  
<221> peptide  
<222> (1)..(372)  
<223> Squirrel Monkey AIPL1 Protein  
  
<400> 78

UTHou-16UTL final.ST25

Met	Asp	Ala	Ala	Leu	Leu	Leu	Asn	Val	Glu	Gly	Val	Lys	Lys	Thr	Ile	1	5	10	15
Leu	His	Gly	Gly	Thr	Gly	Glu	Leu	Pro	Asn	Phe	Ile	Thr	Gly	Ser	Arg	20	25	30	
Val	Ile	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu	Arg	Thr	Val	35	40	45	
Ile	Asp	Asp	Ser	Arg	Glu	Val	Gly	Gln	Pro	Met	His	Ile	Ile	Ile	Gly	50	55	60	
Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu	Leu	Thr	Ser	Met	Arg	65	70	75	80
Val	Arg	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp	Thr	Ile	His	Thr	Gly	Val	85	90	95	
Tyr	Pro	Ile	Leu	Ser	Arg	Ser	Leu	Arg	Gln	Met	Ala	Gln	Gly	Lys	Asp	100	105	110	
Pro	Thr	Glu	Trp	His	Val	His	Thr	Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala	115	120	125	
Tyr	His	Thr	Leu	Gly	Tyr	Glu	Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro	130	135	140	
Gln	Pro	Leu	Ile	Phe	Val	Ile	Glu	Leu	Leu	Gln	Val	Asp	Ala	Pro	Ser	145	150	155	160
Asp	Tyr	Gln	Arg	Glu	Thr	Trp	Asn	Leu	Ser	Asn	His	Glu	Lys	Met	Lys	165	170	175	
Val	Val	Pro	Val	Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Phe	Lys	Leu	Gly	180	185	190	
Arg	Tyr	Glu	Glu	Ala	Ser	Ser	Lys	Tyr	Gln	Glu	Ala	Ile	Ile	Cys	Leu	195	200	205	
Arg	Asn	Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Gln	Trp	Leu	Lys	210	215	220	
Leu	Glu	Lys	Met	Ile	Asn	Thr	Leu	Ile	Leu	Asn	Tyr	Cys	Gln	Cys	Leu	225	230	235	240

UTHou-16UTL final.ST25

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile  
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg  
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln  
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg  
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Trp Ser Pro Ala  
325 330 335

Glu Pro Pro Ala Glu Pro Pro Ala Glu Ser Ser Thr Glu Pro Pro Ala  
340 345 350

Glu Pro Pro Ala Glu Pro Pro Ala Glu Leu Thr Leu Thr Pro Gly His  
355 360 365

Pro Leu Gln His  
370

<210> 79  
<211> 330  
<212> PRT  
<213> Homo sapiens

<220>  
<221> peptide  
<222> (1)..(330)  
<223> Homo sapiens AIP protein sequence

<400> 79

Met Ala Asp Ile Ile Ala Arg Leu Arg Glu Asp Gly Ile Gln Lys Arg  
1 5 10 15

Val Ile Gln Glu Gly Arg Gly Glu Leu Pro Asp Phe Gln Asp Gly Thr  
20 25 30



UTHou-16UTL final.ST25

Lys Ala Thr Phe His Tyr Arg Thr Leu His Ser Asp Asp Glu Gly Thr  
35 40 45

Val Leu Asp Asp Ser Arg Ala Arg Gly Lys Pro Met Glu Leu Ile Ile  
50 55 60

Gly Lys Lys Phe Lys Leu Pro Val Trp Glu Thr Ile Val Cys Thr Met  
65 70 75 80

Arg Glu Gly Glu Ile Ala Gln Phe Leu Cys Asp Ile Lys His Val Val  
85 90 95

Leu Tyr Pro Leu Val Ala Lys Ser Leu Arg Asn Ile Ala Val Gly Lys  
100 105 110

Asp Pro Leu Glu Gly Gln Arg His Cys Cys Gly Val Ala Gln Met Arg  
115 120 125

Glu His Ser Ser Leu Gly His Ala Asp Leu Asp Ala Leu Gln Gln Asn  
130 135 140

Pro Gln Pro Leu Ile Phe His Met Glu Met Leu Lys Val Glu Ser Pro  
145 150 155 160

Gly Thr Tyr Gln Gln Asp Pro Trp Ala Met Thr Asp Glu Glu Lys Ala  
165 170 175

Lys Ala Val Pro Leu Ile His Gln Glu Gly Asn Arg Leu Tyr Arg Glu  
180 185 190

Gly His Val Lys Glu Ala Ala Ala Lys Tyr Tyr Asp Ala Ile Ala Cys  
195 200 205

Leu Lys Asn Leu Gln Met Lys Glu Gln Pro Gly Ser Pro Glu Trp Ile  
210 215 220

Gln Leu Asp Lys Gln Ile Thr Pro Leu Leu Leu Asn Tyr Cys Gln Cys  
225 230 235 240

Lys Leu Val Val Glu Glu Tyr Tyr Glu Val Leu Asp His Cys Ser Ser  
245 250 255

Ile Leu Asn Lys Tyr Asp Asp Asn Val Lys Ala Tyr Phe Lys Arg Gly  
260 265 270

UTHou-16UTL final.ST25

Lys Ala His Ala Ala Val Trp Asn Ala Gln Glu Ala Gln Ala Asp Phe  
275 280 285

Ala Lys Val Leu Glu Leu Asp Pro Ala Leu Ala Pro Val Val Ser Arg  
290 295 300

Glu Leu Arg Ala Leu Glu Ala Arg Ile Arg Gln Lys Asp Glu Glu Asp  
305 310 315 320

Lys Ala Arg Phe Arg Gly Ile Phe Ser His  
325 330

<210> 80  
<211> 330  
<212> PRT  
<213> Mus musculus

<220>  
<221> peptide  
<222> (1)..(330)  
<223> Mouse AIP protein sequence

<400> 80

Met Ala Asp Leu Ile Ala Arg Leu Arg Glu Asp Gly Ile Gln Lys Arg  
1 5 10 15

Val Ile Gln Glu Gly Arg Gly Glu Leu Pro Asp Phe Gln Asp Gly Thr  
20 25 30

Lys Ala Thr Phe His Phe Arg Thr Leu His Ser Asp Asn Glu Gly Ser  
35 40 45

Val Ile Asp Asp Ser Arg Thr Arg Gly Lys Pro Met Glu Leu Ile Val  
50 55 60

Gly Lys Lys Phe Lys Leu Pro Val Trp Glu Thr Ile Val Cys Thr Met  
65 70 75 80

Arg Glu Gly Glu Ile Ala Gln Phe Leu Cys Asp Ile Lys His Val Val  
85 90 95

Leu Tyr Pro Leu Val Ala Lys Ser Leu Arg Asn Ile Ala Glu Gly Lys  
100 105 110

Asp Pro Leu Glu Gly Gln Arg His Cys Cys Gly Ile Ala Gln Met His

UTHou-16UTL final.ST25

115

120

125

Glu His Ser Ser Leu Gly His Ala Asp Leu Asp Ala Leu Gln Gln Asn  
130 135 140

Pro Gln Pro Leu Ile Phe His Ile Glu Met Leu Lys Val Glu Ser Pro  
145 150 155 160

Gly Thr Tyr Gln Gln Asp Pro Trp Ala Met Thr Asp Glu Glu Lys Ala  
165 170 175

Lys Ala Val Pro Val Ile His Gln Glu Gly Asn Arg Leu Tyr Arg Glu  
180 185 190

Gly Gln Val Lys Glu Ala Ala Ala Lys Tyr Tyr Asp Ala Ile Ala Cys  
195 200 205

Leu Lys Asn Leu Gln Met Lys Glu Gln Pro Gly Ser Pro Asp Trp Ile  
210 215 220

Gln Leu Asp Leu Gln Ile Thr Pro Leu Leu Leu Asn Tyr Cys Gln Cys  
225 230 235 240

Lys Leu Val Ala Gln Glu Tyr Tyr Glu Val Leu Asp His Cys Ser Ser  
245 250 255

Ile Leu Asn Lys Tyr Asp Asp Asn Val Lys Ala Tyr Phe Lys Arg Gly  
260 265 270

Lys Ala His Ala Ala Val Trp Asn Ala Gln Glu Ala Gln Ala Asp Phe  
275 280 285

Ala Lys Val Leu Glu Leu Asp Pro Ala Leu Ala Pro Val Val Ser Arg  
290 295 300

Glu Leu Arg Ala Leu Glu Thr Arg Ile Arg Gln Lys Asp Glu Glu Asp  
305 310 315 320

Lys Ala Arg Phe Arg Gly Ile Phe Ser His  
325 330

<210> 81

<211> 328

<212> PRT

<213> Rattus norvegicus

UTHou-16UTL final.ST25

<220>

<221> peptide

<222> (1)..(328)

<223> Rat AIPL1 protein sequence

<400> 81

Met Asp Val Ser Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile  
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg  
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val  
35 40 45

Ile Asp Asp Ser Lys Gln Val Gly Gln Pro Met Asn Ile Ile Ile Gly  
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Thr Leu Leu Thr Ser Met Arg  
65 70 75 80

Leu Gly Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val  
85 90 95

Tyr Pro Met Leu Ser Arg Ser Leu Arg Gln Val Ala Glu Gly Lys Asp  
100 105 110

Pro Thr Ser Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala  
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro  
130 135 140

Gln Pro Leu Ile Phe Leu Ile Glu Leu Leu Gln Val Glu Ala Pro Asn  
145 150 155 160

Glu Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Glu Glu Arg Met Gln  
165 170 175

Ala Val Pro Leu Leu His Gly Glu Gly Asn Arg Leu Tyr Lys Leu Gly  
180 185 190

Arg Tyr Asp Gln Ala Ala Thr Lys Tyr Gln Glu Ala Ile Val Cys Leu  
195 200 205

UTHou-16UTL final.ST25

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Glu Trp Leu Lys  
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu  
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile  
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Met Arg Ala Arg  
260 265 270

Ala His Ala Glu Val Trp Asn Ala Glu Glu Ala Lys Ala Asp Leu Glu  
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Leu Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Ser Arg Leu Ala Asp Lys Gln Glu Glu Glu Arg  
305 310 315 320

Gln Arg Cys Arg Ser Met Leu Gly  
325

<210> 82  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (1)..(12)  
<223> 12 base deletion at Pro351

<400> 82  
tgcagagcca cc

12